

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,324A
Source: PG
Date Processed by STIC: 1/27/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/525,324A

CRF Edit Date:

Edited by:

1/31/06

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

— Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

— Moved responses to same line as heading/numeric identifier, specifically:

✓ Other:

Sequence 14 - used numeral "1" and numeral "0" in amino acid numbering (instead of letter "l" and letter "O")

Sequence 2 - replaced numeral "1" in "Artificial" until letter "l"

Revised 09/09/2003



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/525,324A

DATE: 01/31/2006

TIME: 14:48:13

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01312006\J525324A.raw

3 <110> APPLICANT: SAKI, Mayumi
 4 NONAKA, Hiromi
 5 MIYAJI, Hiromasa
 6 ICHIKAWA, Shunji
 7 TAKASHIMA, Chiemi
 8 MATSUMURA, Tsutomu
 9 ARAI, Hitoshi
 10 SASAKI, Katsutoshi
 11 KOBATAKE, Choei
 12 TSUKUMO, Yukihito
 13 IIDA, Kyoichiro
 14 KUBOYAMA, Takeshi
 15 MANABE, Haruhiko
 17 <120> TITLE OF INVENTION: Agent for prevention and/or treatment of itching
 19 <130> FILE REFERENCE: 506.44793X00
 21 <140> CURRENT APPLICATION NUMBER: US/10/525,324A
 22 <141> CURRENT FILING DATE: 2005-02-22
 24 <150> PRIOR APPLICATION NUMBER: JP 2002/241522
 25 <151> PRIOR FILING DATE: 2002-08-22
 27 <160> NUMBER OF SEQ ID NOS: 20
 29 <170> SOFTWARE: PatentIn Ver 2.1
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 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Synthetic DNA
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 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: Synthetic DNA
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 54 <210> SEQ ID NO: 3
 55 <211> LENGTH: 39
 56 <212> TYPE: DNA
 57 <213> ORGANISM: Artificial Sequence
 59 <220> FEATURE:
 60 <223> OTHER INFORMATION: Synthetic DNA

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62 <400> SEQUENCE: 3
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67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Synthetic DNA
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74 gtaccccccgg gctcgagttt ggacaaacca caactagaa 39
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 40
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
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84 <400> SEQUENCE: 5
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90 <211> LENGTH: 40
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
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106 <213> ORGANISM: Artificial Sequence
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109 <223> OTHER INFORMATION: Synthetic DNA
111 <400> SEQUENCE: 7
112 gccccagaag cttaagtgcc caccatggg 29
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 33
118 <212> TYPE: DNA
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132 <213> ORGANISM: Artificial Sequence
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138 cgaggactct agagggtata taatg 25
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 151 ctaatacgcac tcactatagg g 21
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 154 <211> LENGTH: 362
 155 <212> TYPE: PRT
 156 <213> ORGANISM: Homo sapiens
 158 <400> SEQUENCE: 11
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 160 1 5 10 15
 162 His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu
 163 20 25 30
 165 Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln
 166 35 40 45
 168 Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu
 169 50 55 60
 171 Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His
 172 65 70 75 80
 174 Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile
 175 85 90 95
 177 Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser
 178 100 105 110
 180 Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu
 181 115 120 125
 183 Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr
 184 130 135 140
 186 Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg
 187 145 150 155 160
 189 Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly
 190 165 170 175
 192 Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe
 193 180 185 190
 195 Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val
 196 195 200 205
 198 Arg Gly Ser Val Ser Thr Gln Arg Gln Glu Lys Ala Lys Ile Lys Arg
 199 210 215 220
 201 Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr
 202 225 230 235 240
 204 His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp
 205 245 250 255
 207 Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu
 208 260 265 270
 210 Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu

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Input Set : A:\PTO.AMC.txt

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211	275	280	285
213	Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu		
214	290	295	300
216	Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser		
217	305	310	315
219	Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys		
220	325	330	335
222	Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln		
223	340	345	350
225	Val Gln Leu Lys Met Leu Pro Pro Ala Gln		
226	355	360	
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229	<211> LENGTH: 2932		
230	<212> TYPE: DNA		
231	<213> ORGANISM: Homo sapiens		
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235	ggagtccctc ccctgcccccc attgaaattt ccctccgtc cccaaactta cctctgatct 120		
236	agacacctact cacctccctc ctgtttccctt agactccccc ctgccgtcca cagaccgagc 180		
237	cttttatctt tgtccaccct gtgccagaca cctccctttc cagaacccctc tccttactgg 240		
238	tgacacctact tatctctgtt gctttctggg gtccttaggaa atgcccagcac tcccacccac 300		
239	attgcctgaa ctttccaaca ctcccttagt ggcgtgtgtc ctatctcaac acttcctcat 360		
240	gtatttcttg tgtcttcttag aacattcccc cgccatttatt acttcaatat ggctacacat 420		
241	acttcctaatt tgccctgcaa accatctctt ttcaccatt gcccagcgtat gcttcgtct 480		
242	cctccataaaa cactcccgaa gaccaatttt tgcgtcaccc ccataactccc tcgttgacac 540		
243	actgactcca tacataaacct cttgaaaaaa cctcttttatt aatctcacca tcctccagac 600		
244	ttccctcttg tcataattcc atccctccctc caactttcc ctctcaagct ctggcccttcc 660		
245	cagcccagcc cagccttaccc aacctcatct ctccctgtt gaccacatcc caccatgttc 720		
246	ccctgagcct ccaaggaaagg ggctcagggg gccccatggc ctcccgctcc ctgtggcccc 780		
247	acagccccccg tggccaggg gaagcgcccc agaagccgaa gtgcccacc atg ggc aac 838		
248			Met Gly Asn
249			1
251	cac acg tgg gag ggc tgc cac gtg gac tcg cgc gtg gac cac ctc ttt 886		
252	His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe		
253	5	10	15
255	ccg cca tcc ctc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac 934		
256	Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn		
257	20	25	30
258	.35		
259	tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag 982		
260	Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu		
261	40	45	50
263	ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030		
264	Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile		
265	55	60	65
267	tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg 1078		
268	Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp		
269	70	75	80
271	atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc 1126		
272	Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr		

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273	85	90	95	
275	aat atc tac atc agc atc gcc ttc ctg tgc atc tcg gtg gac cgc	1174		
276	Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser Val Asp Arg			
277	100	105	110	115
279	tac ctg gct gtg gcc cac cca ctc cgc ttc gcc cgc ctg cgc cgc gtc	1222		
280	Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu Arg Arg Val			
281	120	125	130	
283	aag acc gcc gtg gcc gtg agc tcc gtg gtc tgg gcc acg gag ctg ggc	1270		
284	Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr Glu Leu Gly			
285	135	140	145	
287	gcc aac tcc gcg ccc ctg ttc cat gac gag ctc ttc cga gac cgc tac	1318		
288	Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg Asp Arg Tyr			
289	150	155	160	
291	aac cac acc ttc tgc ttt gag aag ttc ccc atg gaa ggc tgg gtg gcc	1366		
292	Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly Trp Val Ala			
293	165	170	175	
295	tgg atg aac ctc tat cgg gtg ttc gtg ggc ttc ctc ttc ccg tgg gcg	1414		
296	Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe Pro Trp Ala			
297	180	185	190	195
299	ctc atg ctg ctg tac cgg ggc atc ctg cgg gcc gtg cgg ggc agc	1462		
300	Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val Arg Gly Ser			
301	200	205	210	
303	gtg tcc acc gag cgc cag gag aag gcc aag atc aag cgg ctg gcc ctc	1510		
304	Val Ser Thr Glu Arg Glu Glu Lys Ala Lys Ile Lys Arg Leu Ala Leu			
305	215	220	225	
307	agc ctc atc gcc atc gtg ctg gtc ttc gcg ccc tat cac gtg ctc	1558		
308	Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr His Val Leu			
309	230	235	240	
311	ttg ctg tcc cgc agc gcc atc tac ctg ggc cgc ccc tgg gac tgc ggc	1606		
312	Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp Asp Cys Gly			
313	245	250	255	
315	tcc gag gag cgc gtc ttt tct gca tac cac agc tga ctg ggt ttc acc	1654		
316	Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu Ala Phe Thr			
317	260	265	270	275
319	agc ctc aac tgt gtg gcg gac ccc atc ctc tac tgc ctg gtc aac gag	1702		
320	Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu Val Asn Glu			
321	280	285	290	
323	ggc gcc cgc agc gat gtg gcc aag gcc ctg cac aac ctg ctc cgc ttt	1750		
324	Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu Arg Phe			
325	295	300	305	
327	ctg gcc agc gac aag ccc cag gag atg gcc aat gcc tcg ctc acc ctg	1798		
328	Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser Leu Thr Leu			
329	310	315	320	
331	gag acc cca ctc acc tcc aag agg aac agc aca gcc aaa gcc atg act	1846		
332	Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys Ala Met Thr			
333	325	330	335	
335	ggc agc tgg gcg gcc act ccg ccc tcc cag ggg gac cag gtg cag ctg	1894		
336	Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln Val Gln Leu			
337	340	345	350	355

VERIFICATION SUMMARY

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Raw Sequence Listing before editing (for reference only)



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/525,324A

DATE: 01/27/2006
TIME: 09:50:49

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\01272006\J525324A.raw

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3 <110> APPLICANT: SAKI, Mayumi
4     NONAKA, Hiromi
5     MIYAJI, Hiromasa
6     ICHIKAWA, Shunji
7     TAKASHIMA, Chiemi
8     MATSUMURA, Tsutomu
9     ARAI, Hitoshi
10    SASAKI, Katsutoshi
11    KOBATAKE, Choei
12    TSUKUMO, Yukihito
13    IIDA, Kyoichiro
14    KUBOYAMA, Takeshi
15    MANABE, Haruhiko
17 <120> TITLE OF INVENTION: Agent for prevention and/or treatment of itching
19 <130> FILE REFERENCE: 506.44793X00
21 <140> CURRENT APPLICATION NUMBER: US/10/525,324A
22 <141> CURRENT FILING DATE: 2005-02-22
24 <150> PRIOR APPLICATION NUMBER: JP 2002/241522
25 <151> PRIOR FILING DATE: 2002-08-22
27 <160> NUMBER OF SEQ ID NOS: 20
29 <170> SOFTWARE: PatentIn Ver 2.1

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ERRORED SEQUENCES

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 448 gtg gac cac ctc ttc cca cca tct ctc tac atc ttc gtc atc ggg gtg 96
 449 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val
 450 20 25 30
 452 ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgg cag gtg 144
 453 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val
 454 35 40 45
 456 cgc caa cac aat gag ctg ggc gtc tac ctg atg aac ttg agc att gca 192
 457 Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala
 458 50 55 60
 460 gac ctg ctg tac atc tgc act ttg ccg ctg tgg gtc gac tac ttc ctc 240

*Does Not Comply
 Corrected Diskette Needed*

P2

RAW SEQUENCE LISTING
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DATE: 01/27/2006
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461 Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu
 462 65 70 75 80
 464 cac cat gac aac tgg atc cac ggc cct ggc tcc tgc aag ctc ttt ggc 288
 465 His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly
 466 85 90 95
 468 ttc atc ttc tac agc aac atc tat atc agc atc gcc ttc ctg tgc tgc 336
 469 Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys
 470 100 105 110
 472 atc tcc gtg gac cgc tac ctg gct gtg gct cat cct ctg cgc ttt gca 384
 473 Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala
 474 115 120 125
 476 cgc ctg cgc cgg gtc aag aca gca gtg gct gtg agc tct gtg gtc tgg 432
 477 Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp
 478 130 135 140
 480 gcc acg gag ctg ggc gcc aat tca gca ccg ctc ttc cat gat gag ctg 480
 481 Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu
 E--> 482 145 150 155 use number 1 ← (160) ← use number "Q"
 E--> 484 ttt cgt gat cgc tac aac cac acc ttc tgc ttt gag aag ttc ccc atg 528
 485 Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met
 W--> 486 165 170 175
 E--> 488 gag cgt tgg gtg gcc tgg atg aat ctg tac cgc gtc ttt gtg ggc ttc 576
 489 Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe
 490 180 185 190
 E--> 492 ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgt ggc atc ctg agg 624
 493 Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg
 494 195 200 205
 E--> 496 gca gtg cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc 672
 497 Ala Val Gln Ser Ser Val Ser Thr Glu Arg Glu Glu Lys Val Lys Ile
 498 210 215 220
 E--> 500 aaa cgt ctg gcc ctg agc ctc atc gcc att gtg ctg gtg tgc ttt gcg 720
 501 Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala
 502 225 230 235 240
 E--> 504 cct tac cat gct ctc ctg tct cgc agc gcc gtc tac ctg ggc cgg 768
 505 Pro Tyr His Ala Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg
 506 245 250 255
 E--> 508 ccc tgg gac tgt ggc ttc gag gag cga gtc ttt tct gcc tac cac agc 816
 509 Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser
 510 260 265 270
 E--> 512 tcc ctg gcc ttc acc agc ctc aat tgt gtg gct gac ccc atc ctc tac 864
 513 Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr
 514 275 280 285
 E--> 516 tgc ctg gtc aac gag ggt gcc cgc agt gat gtg gcc aag gcc ctg cac 912
 517 Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His
 518 290 295 300
 E--> 520 aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat 960
 521 Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn
 522 305 310 315 320
 E--> 524 gct tcc ctc acc ctg gag aca ccc ttg acc tcc aag agg agc acc acc 1008
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526 325 330 335
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 529 Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly
 530 340 345 350
E--> 532 gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga 1098
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E--> 534 355 360 365
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E--> 640 <2T3> Rattus norvegicus
E--> 642
 642 <400> SEQUENCE: 18
L2137
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 645 1 5 10 15
 647 gtg gac cac ctc ttc cca cca tcc ctc tac atc ttc gtc atc ggg gtg 96
 648 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val
 649 20 25 30
 651 ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgc cag gtg 144
 652 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val
 653 35 40 45
 655 cgc cag cgc aat gag ctg ggc gtc tac ctg atg aac ttg agc atc gca 192
 656 Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala
 657 50 55 60
 659 gac ctg ctg tac atc tgt acg ctg ccg ctg tgg gtc gac tac ttc ctc 240
 660 Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu
 661 65 70 75 80
 663 cac cat gac aac tgg atc cac ggc ccc ggc tcc tgc aag ctc ttt ggc 288
 664 His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly
 665 85 90 95
 667 ttc atc ttc tac agc aac atc tac atc agc atc gcc ttc ctg tgc tgc 336
 668 Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys
 669 100 105 110
 671 atc tcc gtg gac cgc tac ctg gct gtg gcc cat ccg ctg cgc ttt gcg 384
 672 Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala
 673 115 120 125
 675 cgc ctg cgc cgg gtc aag aca gca gta gct gtg agc tcc gtg gtc tgg 432
 676 Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp
 677 130 135 140
 679 gcc acc gag cta ggc gcc aac tcg gca ccg ctc ttt cat gac gag ctc 480
 680 Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu
 681 145 150 155 160
 683 ttt cgt gat cgc tac aac cac acc ttc tgc ttc gag aag ttc ccc atg 528
 684 Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met
 685 165 170 175
 687 gag cgc tgg gtg gcc tgg atg aac ctg tac cgc gtc ttt gtg ggg ttc 576
 688 Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe
 689 180 185 190

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\01272006\J525324A.raw

691	ctc	tcc	ccc	tgg	gca	ctc	atg	ttg	ctg	tgc	tac	cgc	ggc	atc	ctg	cg	624
692	Leu	Phe	Pro	Trp	Ala	Leu	Met	Leu	Leu	Cys	Tyr	Arg	Gly	Ile	Leu	Arg	
693							195		200						205		
695	gcc	gta	cag	agc	agt	gtg	tcc	acc	gag	cgc	cag	gag	aaa	gtc	aag	atc	672
696	Ala	Val	Gln	Ser	Ser	Val	Ser	Thr	Glu	Arg	Gln	Glu	Lys	Val	Lys	Ile	
697							210		215					220			
699	aaa	cgc	ctg	gcc	ctg	agc	ctc	atc	gcc	atc	gtg	ctg	gtg	tgc	ttt	gca	720
700	Lys	Arg	Leu	Ala	Leu	Ser	Leu	Ile	Ala	Ile	Val	Leu	Val	Cys	Phe	Ala	
701	225						230			235					240		
703	ccc	tac	cat	gct	ctc	ttg	ctg	tct	cgc	agc	gct	gtc	tat	ctg	ggc	cg	768
704	Pro	Tyr	His	Ala	Leu	Leu	Leu	Ser	Arg	Ser	Ala	Val	Tyr	Leu	Gly	Arg	
705							245			250				255			
707	ccc	tgg	gac	tgt	ggc	ttc	gag	gag	cga	gtc	ttc	tct	gcc	tac	cac	agc	816
708	Pro	Trp	Asp	Cys	Gly	Phe	Glu	Glu	Arg	Val	Phe	Ser	Ala	Tyr	His	Ser	
709							260			265				270			
711	tcc	cta	gcc	tcc	acc	agc	ctc	aat	tgc	gtg	gct	gac	ccc	atc	ctc	tac	864
712	Ser	Leu	Ala	Phe	Thr	Ser	Leu	Asn	Cys	Val	Ala	Asp	Pro	Ile	Leu	Tyr	
713							275		280				285				
715	tgc	ctg	gtc	aac	gag	ggt	gcc	cgt	agt	gac	gtg	gcc	aaa	gcc	ctg	cac	912
716	Cys	Leu	Val	Asn	Glu	Gly	Ala	Arg	Ser	Asp	Val	Ala	Lys	Ala	Leu	His	
717							290		295				300				
719	aac	ctc	ctc	cg	ttc	ctg	gcc	agc	aac	aag	ccc	cag	gag	atg	gcc	aat	960
720	Asn	Leu	Leu	Arg	Phe	Leu	Ala	Ser	Asn	Lys	Pro	Gln	Glu	Met	Ala	Asn	
721	305						310			315				320			
723	gct	tcc	ctc	acc	ctg	gag	aca	cca	ttg	acc	tcc	aag	agg	agc	acc		1008
724	Ala	Ser	Leu	Thr	Leu	Glu	Thr	Pro	Leu	Thr	Ser	Lys	Arg	Ser	Thr	Thr	
725							325			330				335			
727	ggc	aaa	acg	tct	ggg	gct	gtc	tgg	gca	gtg	cct	ccc	act	gcc	cag	gg	1056
728	Gly	Lys	Thr	Ser	Gly	Ala	Val	Trp	Ala	Val	Pro	Pro	Thr	Ala	Gln	Gly	
729							340			345				350			
731	gac	cag	gtg	cca	ctg	aag	gtg	ctg	ctg	ccc	ccg	gca	cag	tga		1098	
732	Asp	Gln	Val	Pro	Leu	Lys	Val	Leu	Leu	Pro	Pro	Ala	Gln				
733							355			360				365			

VERIFICATION SUMMARY DATE: 01/27/2006
PATENT APPLICATION: US/10/525,324A TIME: 09:50:50

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\01272006\J525324A.raw

L:46 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:482 SEQ:14
L:482 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:484 M:254 E: No. of Bases conflict, LENGTH:Input:528 Counted:530 SEQ:14
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:488 M:254 E: No. of Bases conflict, LENGTH:Input:576 Counted:578 SEQ:14
L:492 M:254 E: No. of Bases conflict, LENGTH:Input:624 Counted:626 SEQ:14
L:496 M:254 E: No. of Bases conflict, LENGTH:Input:672 Counted:674 SEQ:14
L:500 M:254 E: No. of Bases conflict, LENGTH:Input:720 Counted:722 SEQ:14
L:504 M:254 E: No. of Bases conflict, LENGTH:Input:768 Counted:770 SEQ:14
L:508 M:254 E: No. of Bases conflict, LENGTH:Input:816 Counted:818 SEQ:14
L:512 M:254 E: No. of Bases conflict, LENGTH:Input:864 Counted:866 SEQ:14
L:516 M:254 E: No. of Bases conflict, LENGTH:Input:912 Counted:914 SEQ:14
L:520 M:254 E: No. of Bases conflict, LENGTH:Input:960 Counted:962 SEQ:14
L:524 M:254 E: No. of Bases conflict, LENGTH:Input:1008 Counted:1010 SEQ:14
L:528 M:254 E: No. of Bases conflict, LENGTH:Input:1056 Counted:1058 SEQ:14
L:532 M:254 E: No. of Bases conflict, LENGTH:Input:1098 Counted:1100 SEQ:14
L:534 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1098 Found:1100 SEQ:14
L:640 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:642 M:282 E: Numeric Field Identifier Missing, <213> is required.